

T300X

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: COLOTTA, Francesco
MUZIO, Marta
MANTOVANI, Alberto

(ii) TITLE OF INVENTION: INTERLEUKIN-1 ANTAGONIST, DNA ENCODING SAME,
AND ANTIBODIES THERETO

(iii) NUMBER OF SEQUENCES: 17

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: BROWDY AND NEIMARK
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(C) CITY: Washington
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(E) COUNTRY: USA
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/476,860
(B) FILING DATE: 07-JUN-1995

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: IT MI 94 A 002097
(B) FILING DATE: 13-OCT-1994

(viii) ATTORNEY/AGENT INFORMATION:

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(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(D) OTHER INFORMATION: RT-PCR oligonucleotide named IRA5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTGACTTGTA TGAAGAAGGA GGTGG

25

30

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:
(D) OTHER INFORMATION: RT-PCR oligonucleotide corresponding to 60-79 of B-actin

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GCGCTCGTCG TCGACAAACGG

20

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:
(D) OTHER INFORMATION: RT-PCR backward oligonucleotide complementary to 430-449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GATAGACAAAC GTACATGGCT G

21

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:
(D) OTHER INFORMATION: Sequence of sIL-1ra not in common

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 24..86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GAATTCCGGG CTGCAGTCAC AGA ATG GAA ATC TGC AGA GGC CTC CGC AGT
Met Glu Ile Cys Arg Gly Leu Arg Ser

1 5

50

CAC CTA ATC ACT CTC CTC CTC TTC CTG TTC CAT TCA G
His Leu Ile Thr Leu Leu Leu Phe Leu Phe His Ser
10 15 20

87

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Met Glu Ile Cys Arg Gly Leu Arg Ser His Leu Ile Thr Leu Leu Leu
1 5 10 15
Phe Leu Phe His Ser
20

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:
(D) OTHER INFORMATION: Sequence of intracellular IL-1ra
typeI not in common

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 33..41

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CAGAAGACCT CCTGTCCTAT GAGGCCCTCC CC ATG GCT TTA G
Met Ala Leu
1

42

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(D) OTHER INFORMATION: Sequence of intracellular IL-1ra typeII not in common

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 33..104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

| | |
|---|-----|
| CAGAAGACCT CCTGTCCTAT GAGGCCCTCC CC ATG GCT TTA GCT GAC TTG TAT | 53 |
| Met Ala Leu Ala Asp Leu Tyr | |
| 1 5 | |
| GAA GAA GGA GGT GGA GGA GGA GAA GGT GAA GAC AAT GCT GAC TCA | 101 |
| Glu Glu Gly Gly Gly Gly Glu Gly Asp Asn Ala Asp Ser | |
| 10 15 20 | |
| AAG G | 105 |
| Lys | |

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

| | |
|---|--|
| Met Ala Leu Ala Asp Leu Tyr Glu Glu Gly Gly Gly Gly Gly Glu | |
| 1 5 10 15 | |
| Gly Glu Asp Asn Ala Asp Ser Lys | |
| 20 | |

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 474 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(D) OTHER INFORMATION: Common IL-1ra sequence; a nucleotide G was added in the first position, for computer program reason, in order to encode the first amino acid Glu and further in order to avoid the creation of a stop codon in the inner region of the sequence

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

| | |
|--|-----|
| GAG ACG ATC TGC CGA CCC TCT GGG AGA AAA TCC AGC AAG ATG CAA GCC Glu Thr Ile Cys Arg Pro Ser Gly Arg Lys Ser Ser Lys Met Gln Ala | 48 |
| 1 5 10 15 | |
| TTC AGA ATC TGG GAT GTT AAC CAG AAG ACC TTC TAT CTG AGG AAC AAC Phe Arg Ile Trp Asp Val Asn Gln Lys Thr Phe Tyr Leu Arg Asn Asn | 96 |
| 20 25 30 | |
| CAA CTA GTT GCT GGA TAC TTG CAA GGA CCA AAT GTC AAT TTA GAA GAA Gln Leu Val Ala Gly Tyr Leu Gln Gly Pro Asn Val Asn Leu Glu Glu | 144 |
| 35 40 45 | |
| AAG ATA GAT GTG GTA CCC ATT GAG CCT CAT GCT CTG TTC TTG GGA ATC Lys Ile Asp Val Val Pro Ile Glu Pro His Ala Leu Phe Leu Gly Ile | 192 |
| 50 55 60 | |
| CAT GGA GGG AAG ATG TGC CTG TCC TGT GTC AAG TCT GGT GAT GAG ACC His Gly Gly Lys Met Cys Leu Ser Cys Val Lys Ser Gly Asp Glu Thr | 240 |
| 65 70 75 80 | |
| AGA CTC CAG CTG GAG GCA GTT AAC ATC ACT GAC CTG AGC GAG AAC AGA Arg Leu Gln Leu Glu Ala Val Asn Ile Thr Asp Leu Ser Glu Asn Arg | 288 |
| 85 90 95 | |
| AAG CAG GAC AAG CGC TTC GCC TTC ATC CGC TCA GAC AGT GGC CCC ACC Lys Gln Asp Lys Arg Phe Ala Phe Ile Arg Ser Asp Ser Gly Pro Thr | 336 |
| 100 105 110 | |
| ACC AGT TTT GAG TCT GCC GCC TGC CCC GGT TGG TTC CTC TGC ACA GCG Thr Ser Phe Glu Ser Ala Ala Cys Pro Gly Trp Phe Leu Cys Thr Ala | 384 |
| 115 120 125 | |
| ATG GAA GCT GAC CAG CCC GTC AGC CTC ACC AAT ATG CCT GAC GAA GGC Met Glu Ala Asp Gln Pro Val Ser Leu Thr Asn Met Pro Asp Glu Gly | 432 |
| 130 135 140 | |
| GTC ATG GTC ACC AAA TTC TAC TTC CAG GAG GAC GAG TAGTAC Val Met Val Thr Lys Phe Tyr Phe Gln Glu Asp Glu | 474 |
| 145 150 155 | |

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

| | |
|--|--|
| Glu Thr Ile Cys Arg Pro Ser Gly Arg Lys Ser Ser Lys Met Gln Ala 1 5 10 15 | |
| Phe Arg Ile Trp Asp Val Asn Gln Lys Thr Phe Tyr Leu Arg Asn Asn | |
| 20 25 30 | |
| Gln Leu Val Ala Gly Tyr Leu Gln Gly Pro Asn Val Asn Leu Glu Glu 35 40 45 | |

Lys Ile Asp Val Val Pro Ile Glu Pro His Ala Leu Phe Leu Gly Ile
 50 55 60

His Gly Gly Lys Met Cys Leu Ser Cys Val Lys Ser Gly Asp Glu Thr
 65 70 75 80

Arg Leu Gln Leu Glu Ala Val Asn Ile Thr Asp Leu Ser Glu Asn Arg
 85 90 95

Lys Gln Asp Lys Arg Phe Ala Phe Ile Arg Ser Asp Ser Gly Pro Thr
 100 105 110

Thr Ser Phe Glu Ser Ala Ala Cys Pro Gly Trp Phe Leu Cys Thr Ala
 115 120 125

Met Glu Ala Asp Gln Pro Val Ser Leu Thr Asn Met Pro Asp Glu Gly
 130 135 140

Val Met Val Thr Lys Phe Tyr Phe Gln Glu Asp Glu
 145 150 155

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

- (D) OTHER INFORMATION: A portion of the intracellular IL-1ra typeII not in common

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Ala Asp Leu Tyr Glu Glu Gly Gly Gly Gly Glu Gly Glu Asp
 1 5 10 15

Asn Ala Asp Ser Lys
 20

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 579 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (D) OTHER INFORMATION: Intracellular IL-1ra typeII

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 34..573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

| | |
|--|-----|
| CAGAAGGACC TCCTGTCCCTA TGAGGCCCTC CCC ATG GCT TTA GCT GAC TTG TAT Met Ala Leu Ala Asp Leu Tyr | 54 |
| 1 5 | |
| GAA GAA GGA GGT GGA GGA GGA GAA GGT GAA GAC AAT GCT GAC TCA Glu Glu Gly Gly Gly Gly Glu Gly Glu Asp Asn Ala Asp Ser | 102 |
| 10 15 20 | |
| AAG GAG ACG ATC TGC CGA CCC TCT GGG AGA AAA TCC AGC AAG ATG CAA Lys Glu Thr Ile Cys Arg Pro Ser Gly Arg Lys Ser Ser Lys Met Gln | 150 |
| 25 30 35 | |
| GCC TTC AGA ATC TGG GAT GTT AAC CAG AAG ACC TTC TAT CTG AGG AAC Ala Phe Arg Ile Trp Asp Val Asn Gln Lys Thr Phe Tyr Leu Arg Asn | 198 |
| 40 45 50 55 | |
| AAC CAA CTA GTT GCT GGA TAC TTG CAA GGA CCA AAT GTC AAT TTA GAA Asn Gln Leu Val Ala Gly Tyr Leu Gln Gly Pro Asn Val Asn Leu Glu | 246 |
| 60 65 70 | |
| GAA AAG ATA GAT GTG GTA CCC ATT GAG CCT CAT GCT CTG TTC TTG GGA Glu Lys Ile Asp Val Val Pro Ile Glu Pro His Ala Leu Phe Leu Gly | 294 |
| 75 80 85 | |
| ATC CAT GGA GGG AAG ATG TGC CTG TCC TGT GTC AAG TCT GGT GAT GAG Ile His Gly Gly Lys Met Cys Leu Ser Cys Val Lys Ser Gly Asp Glu | 342 |
| 90 95 100 | |
| ACC AGA CTC CAG CTG GAG GCA GTT AAC ATC ACT GAC CTG AGC GAG AAC Thr Arg Leu Gln Leu Glu Ala Val Asn Ile Thr Asp Leu Ser Glu Asn | 390 |
| 105 110 115 | |
| AGA AAG CAG GAC AAG CGC TTC GCC TTC ATC CGC TCA GAC AGT GGC CCC Arg Lys Gln Asp Lys Arg Phe Ala Phe Ile Arg Ser Asp Ser Gly Pro | 438 |
| 120 125 130 135 | |
| ACC ACC AGT TTT GAG TCT GCC GCC CCC GGT TGG TTC CTC TGC ACA Thr Thr Ser Phe Glu Ser Ala Ala Cys Pro Gly Trp Phe Leu Cys Thr | 486 |
| 140 145 150 | |
| GCG ATG GAA GCT GAC CAG CCC GTC AGC CTC ACC AAT ATG CCT GAC GAA Ala Met Glu Ala Asp Gln Pro Val Ser Leu Thr Asn Met Pro Asp Glu | 534 |
| 155 160 165 | |
| GGC GTC ATG GTC ACC AAA TTC TAC TTC CAG GAG GAC GAG TAGTAC Gly Val Met Val Thr Lys Phe Tyr Phe Gln Glu Asp Glu | 579 |
| 170 175 180 | |

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Met Ala Leu Ala Asp Leu Tyr Glu Glu Gly Gly Gly Gly Gly Glu
1 5 10 15

Gly Glu Asp Asn Ala Asp Ser Lys Glu Thr Ile Cys Arg Pro Ser Gly
20 25 30

Arg Lys Ser Ser Lys Met Gln Ala Phe Arg Ile Trp Asp Val Asn Gln
35 40 45

Lys Thr Phe Tyr Leu Arg Asn Asn Gln Leu Val Ala Gly Tyr Leu Gln
50 55 60

Gly Pro Asn Val Asn Leu Glu Glu Lys Ile Asp Val Val Pro Ile Glu
65 70 75 80

Pro His Ala Leu Phe Leu Gly Ile His Gly Gly Lys Met Cys Leu Ser
85 90 95

Cys Val Lys Ser Gly Asp Glu Thr Arg Leu Gln Leu Glu Ala Val Asn
100 105 110

Ile Thr Asp Leu Ser Glu Asn Arg Lys Gln Asp Lys Arg Phe Ala Phe
115 120 125

Ile Arg Ser Asp Ser Gly Pro Thr Thr Ser Phe Glu Ser Ala Ala Cys
130 135 140

Pro Gly Trp Phe Leu Cys Thr Ala Met Glu Ala Asp Gln Pro Val Ser
145 150 155 160

Leu Thr Asn Met Pro Asp Glu Gly Val Met Val Thr Lys Phe Tyr Phe
165 170 175

Gln Glu Asp Glu
180

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTTGAGTCAG CATTGTCTTC A

21

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTGACTTGTA TGAAGAAGGA GGTGG

25

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ala Asp Leu Tyr Glu Glu Gly Gly Gly Gly Gly Glu Glu Asp
1 5 10 15

Asn Ala Asp Ser Lys
20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

| | |
|--|-----|
| CAGAAAGACCT CCTGTCCTAT GAGGCCCTCC CCATGGCTTT AGGTAAGCTC CTTCCACTCT | 60 |
| CATTTTTCA CCTGAGAAAT GAGAGAGGAA AATGTCTACA ATTGGTGTGTT ATCAAATGCT | 120 |
| TTCAGGCTCT GGTGAGCAAG CGTCCAGGAA AATGTCAAGC GCATGGAGCT CCAGGCCTGT | 180 |
| CTGGGGGATC TGGGCACGGG GAGGCATCCA TGGGAGACCA TGCAGGCACT CTGAGGCAGG | 240 |
| GGCTGCAAGC TAGTGCCTGC TGGGGCAGCA GGTGAACAGA GAGGTGTAAC TGCTGTGACA | 300 |
| GAAGTCATGG AGTCCTTGGG GTGTGAGGGT CATTTCAC TGTTGATAGA ATAGGGAAAT | 360 |
| TGGTGAATA GCCCTGTTAA ATGAGAGAAA GAACAGTGTG AGCTCAATGA GAAATACTAA | 420 |
| TAGAATGTGG CACTGAGCCA CAAGGTCTGA GGGTTGATTG ATAAGGAAGG GTGGGGACTG | 480 |
| TGGAGAATTG AGGGCTTGGC ACAGGTCACT TCCACCAAGT GTCACAAGAG AATGCAGGCT | 540 |
| CAGGTGGCCA GAACTTCTCG CTTTCCAGA AGAGTCCGAT ATTCTGATTT CATTATATAT | 600 |
| AGTATTCTGA TTAAACCAGA CAATAAAGCA AGCAGATAAA ATATTTAAAG TATAAGCTGC | 660 |
| CAGTTGCAA CCTCCGGTTA GGATTTGTGT GGGGCAAAGA AAAAAACTCT CAGGATCATT | 720 |
| GGTATGTAGA CTCTAATTAA AAGTTCTAA TTTAAAATTG GCCCCTGAGG CTGGCGTGG | 780 |
| TGGCTCACAC CTGTAATCCC AGCATTGG GAGGCCAAGG TGGGTGGATC TCTTGAGGTC | 840 |

| | | | | | | |
|------------|------------|------------|-------------|-------------|-------------|------|
| AAGAGTTCAA | GGCCTGCCTG | GCCAACATGG | TGAAACCCTG | TCTCTATTAA | AAATACAAAA | 900 |
| ATTAGCTGGG | CATGGTGGTG | CATGTCTGCA | ATCTTAGCTA | CTTGGGTAGC | TAAGGCAGGA | 960 |
| GAATTGCTGG | AACCCGGGAG | GTAGAGGTTG | CAGTGAATGG | AGATCACACC | ACTGCACTCC | 1020 |
| AGTCTGGGCA | ATAGAGAGAG | ACGCTCTCTC | TAAAAAAA | TATGTAAAGA | TAAATAAAAT | 1080 |
| GAAATAAAAT | AGGCCTCTAA | TGAGCAGGCC | ATTCTCCTTT | CTGGTCTTA | CTTCCTTGC | 1140 |
| ACTCCTTCT | GGGTGTTAAG | AGGAGGTCTA | GAGGAAGCTG | GACAACCTT | AGCTTGTAGT | 1200 |
| AAGCACAGTG | GAAGTATCAG | CTCTTAATGG | GTCATGGACA | CGTTACGAAG | CTAGGCCCG | 1260 |
| TGCTGAGCAC | TTTACATGGT | TTATCCCCT | GAACCCCTCTC | AATAACCCCTA | TGAGGAAGGG | 1320 |
| CTATTATTGC | TCACATTTTC | AGAAGAGGAA | ATGGATATAG | AGAGATTAGA | TAATTTGCC | 1380 |
| ATGGCCAGAC | AGCTAGTATA | AGAGGAGGAG | GTGGATTGAC | TGCAGACATT | CTGTCTTCAA | 1440 |
| ACCACTACAC | TATGCTATGG | AGGCACAGAG | ACTTAATGAA | ATCATGGAGA | GGGGAAATTGC | 1500 |
| TTTGTCAACC | ACAAGCAGTT | ATTCCGGGGG | CAGCAGATCC | TCCCCTGTCC | CCCAGTGGTA | 1560 |
| CAATGGTCCC | TGGTGGGTTG | TGCTACAATG | TTAGCCCCT | GTCTTATGTG | TTTTCAAAT | 1620 |
| GTGTAAAGTA | GGATGCTGGA | ACCACTCTTA | GAACCAGATA | CCAATACATT | GTGAAGAAAT | 1680 |
| AAATCTCTGT | GCTTAAAAC | GGTTCATCCC | AAAATATTTT | GAACGTACAC | ACAATAGGTG | 1740 |
| CTAAATAAT | GTGTGTTAAC | TTGAATTGGA | TTGAATTGG | AAAAAAAGTG | CAATAAGCTT | 1800 |
| AGTGAAGACA | CCATGTTCCC | TGGGTAGAGG | AACCACATTC | TCCATATAAG | GCCAGGAGTA | 1860 |
| TGGGAGGTAT | CAATGTTGC | CCAGCACAGA | ACAGGGTGCC | AAGAAGAGAA | AAGTTGACGG | 1920 |
| GGTGCATACT | CTGACTGGAA | ACTGGAAGGG | TGAGAACAGA | GGGTAAAGGA | TAGAGATGGA | 1980 |
| ACCATGTGCA | TACACTTTGT | GTTACCTTGG | ACAAGTCATT | CATTTCTCTG | GACCTCTGCT | 2040 |
| TTCTCTCTAC | ACAATGGGGT | CCCACCACTT | CCCTTACAGC | TGACTTGTAT | GAAGAAGGAG | 2100 |
| GTGGAGGAGG | AGGAGAAGGT | GAAGACAATG | CTGACTCAA | GGGTAAATT | TTTTAGGAT | 2160 |
| CCAAGTTGA | AAACAATTTT | AGGCTACTAG | ATATGAACAA | CATCTGATT | ATGTAGTTGA | 2220 |
| AGGAAATTAA | AGATGAATGG | TTAATTAAA | AATTAATCAG | AATGAAAACG | ATTGATTACT | 2280 |
| AATATATCTG | CAATGGTTA | TTTCCTGAG | TGGCAGACTC | ACTAAGGTT | TTGAATACTC | 2340 |
| CTGTGTGATT | GCTCTATGTA | TGTATGTATG | TATGTATGTA | TGCATGTATC | TATCTATCTG | 2400 |
| TTGTCTAATA | GAATGGATCA | CATCTCTGCT | AATAAAAACA | CTACACTGGC | AGGGTACAAT | 2460 |
| TATAATCATT | AACTGTGCCT | GGAATTGCA | GCAGCAGCCA | CCAGAGGTAC | CAGTGCCCTT | 2520 |
| TAAGGGTTCA | TAATTTAGAA | TAATCCAATT | ATCTGAGTT | TTCAGGGACT | GAGGGGTTG | 2580 |
| GCAAGGTGTA | GAACCTTCAG | TAATAAAGTC | AAGAAAGTCC | TGGACAAACC | AAGGTAGTTG | 2640 |
| GTCACTCTAG | TCCATAACCA | GGTAAAGAGC | TTTCCCTGTA | ACCTGTGTAA | GGTTTTAGAA | 2700 |
| TCATTTCTTT | CCTTATTACC | AAAAATCCTC | CCCAAATTTT | CAAGAAATT | TGAACTAAAT | 2760 |

| | | | | | | |
|-------------|------------|------------|------------|-------------|-------------|------|
| AGTTACTCTA | TGAGATAGGA | GTTCAGCCCC | AAAGAAACAC | CATAAGAACAA | AATATAATTCA | 2820 |
| TTGCTTATGT | TAACCATGCA | ATGAAGCAGA | GAGAAAAAGT | CAGTGGCCTC | TTTAGGAGGA | 2880 |
| CTGTAGTGTG | GGAAGAAATA | ACTAAACTGG | GTTTCAATCC | TGGCCTGGCC | AGGATCTGGA | 2940 |
| GCAAGTGAGT | TAATCTTCA | AAGCCTTGAG | TAGTTTATAA | AAGAATGGCC | ACTCCATAGA | 3000 |
| CAGAGTAGGCC | TGAACCTTGA | GTTCTTCTAT | AAAGTCACTA | TGAATTTATA | CTCATTGAA | 3060 |
| AAGTGGGTGT | CAATATGTCT | GTCCACTTTG | CACAGCTGTT | ATGTGGACAA | AAGGAGATCT | 3120 |
| GTGTGAAAAGT | GTAACACAGA | GCCTAAACTA | TAACAGGTAA | GCAACACAGT | TGTCCC | 3176 |